RAW SEQUENCE LISTING   DATE: 10/03/2001
PATENT APPLICATION: US/09/762,261A   TIME: 08:45:06

Input Set : A:\Hj5001us.app
Output Set: N:\CRF3\10032001\I762261A.raw

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 3 <110> APPLICANT: Quinnan, Gerald V.
 4         Zhang, Peng Fei
 6 <120> TITLE OF INVENTION: Expression and Characterization of HIV-1 Envelope
 7         Protein Associated with a Broadly Reactive Neutralizing
 8         Antibody Response
10 <130> FILE REFERENCE: 44508-5001-US
12 <140> CURRENT APPLICATION NUMBER: US 09/762,261A
13 <141> CURRENT FILING DATE: 2001-02-05
15 <150> PRIOR APPLICATION NUMBER: US 60/095,267
16 <151> PRIOR FILING DATE: 1998-08-04
18 <150> PRIOR APPLICATION NUMBER: PCT/US99/17596
19 <151> PRIOR FILING DATE: 1999-08-04
21 <160> NUMBER OF SEQ ID NOS: 4
23 <170> SOFTWARE: PatentIn Ver. 2.1
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 866
27 <212> TYPE: PRT
28 <213> ORGANISM: Human immunodeficiency virus type 1
30 <220> FEATURE:
31 <223> OTHER INFORMATION: R2 strain envelope protein (gp 160)
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34 Met Arg Val Lys Gly Ile Arg Arg Asn Tyr Gln His Trp Trp Gly Trp
35  1               5                  10                  15
37 Gly Thr Met Leu Leu Gly Leu Leu Met Ile Cys Ser Ala Thr Glu Lys
38              20                  25                  30
40 Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala Thr
41          35                  40                  45
43 Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu Ala
44      50                  55                  60
46 His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro
47  65                  70                  75                  80
49 Gln Glu Val Glu Leu Val Asn Val Thr Glu Asn Phe Asn Met Trp Lys
50              85                  90                  95
52 Asn Asn Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp Asp
53              100                 105                 110
55 Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Thr Leu
56          115                 120                 125
58 Asn Cys Thr Asp Leu Arg Asn Thr Thr Asn Thr Asn Asn Ser Thr Asp
59      130                 135                 140
61 Asn Asn Asn Ser Asn Ser Glu Gly Thr Ile Lys Gly Gly Glu Met Lys
62 145                 150                 155                 160
64 Asn Cys Ser Phe Asn Ile Ala Thr Ser Ile Gly Asp Lys Met Gln Lys
65                  165                 170                 175
67 Glu Tyr Ala Leu Leu Tyr Lys Leu Asp Ile Glu Pro Ile Asp Asn Asp
68              180                 185                 190
70 Asn Thr Ser Tyr Arg Leu Ile Ser Cys Asn Thr Ser Val Ile Thr Gln
71          195                 200                 205
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 73 Ala Cys Pro Lys Ile Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala
 74         210                 215                 220
 76 Pro Ala Gly Phe Ala Ile Leu Lys Cys Asn Asp Lys Lys Phe Ser Gly
 77 225                 230                 235                 240
 79 Lys Gly Ser Cys Lys Asn Val Ser Thr Val Gln Cys Thr His Gly Ile
 80                 245                 250                 255
 82 Arg Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu
 83             260                 265                 270
 85 Glu Glu Val Val Ile Arg Ser Glu Asn Phe Thr Asn Asn Ala Lys Thr
 86             275                 280                 285
 88 Ile Ile Val Gln Leu Arg Glu Pro Val Lys Ile Asn Cys Ser Arg Pro
 89         290                 295                 300
 91 Asn Asn Asn Thr Arg Lys Ser Ile Pro Met Gly Pro Gly Arg Ala Phe
 92 305                 310                 315                 320
 94 Tyr Thr Thr Gly Gln Ile Ile Gly Asp Ile Arg Gln Ala His Cys Asn
 95                 325                 330                 335
 97 Ile Ser Lys Thr Asn Trp Thr Asn Ala Leu Lys Gln Val Val Glu Lys
 98             340                 345                 350
100 Leu Gly Glu Gln Phe Asn Lys Thr Lys Ile Val Phe Thr Asn Ser Ser
101             355                 360                 365
103 Gly Gly Asp Pro Glu Ile Val Thr His Ser Phe Asn Cys Ala Gly Glu
104         370                 375                 380
106 Phe Phe Tyr Cys Asn Thr Thr Gln Leu Phe Asp Ser Ile Trp Asn Ser
107 385                 390                 395                 400
109 Glu Asn Gly Thr Trp Asn Ile Thr Arg Gly Leu Asn Asn Thr Gly Arg
110                 405                 410                 415
112 Asn Asp Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln Ile Ile Asn Arg
113             420                 425                 430
115 Trp Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Lys Gly Asn
116             435                 440                 445
118 Ile Ser Cys Ser Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly
119         450                 455                 460
121 Gly Lys Asp Asp Asn Ser Arg Asp Gly Asn Glu Thr Phe Arg Pro Gly
122 465                 470                 475                 480
124 Gly Gly Asp Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr Lys
125             485                 490                 495
127 Val Val Lys Ile Glu Pro Leu Gly Val Ala Pro Thr Lys Ala Lys Arg
128             500                 505                 510
130 Arg Val Val Gln Arg Glu Glu Arg Ala Val Gly Leu Gly Ala Met Phe
131         515                 520                 525
133 Ile Gly Phe Leu Gly Ala Ala Gly Ser Thr Met Gly Ala Ala Ser Val
134         530                 535                 540
136 Thr Leu Thr Val Gln Ala Arg Gln Leu Leu Ser Gly Ile Val Gln Gln
137 545                 550                 555                 560
139 Gln Ser Asn Leu Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln
140                 565                 570                 575
142 Leu Thr Val Trp Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala Val
143             580                 585                 590
145 Glu Arg Tyr Leu Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser
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146           595                    600                     605
148 Gly Lys Leu Ile Cys Thr Thr Thr Val Pro Trp Asn Ala Ser Trp Ser
149         610                 615                  620
151 Lys Asn Lys Thr Leu Glu Ala Ile Trp Asn Asn Met Thr Trp Met Gln
152 625                 630                  635                  640
154 Trp Asp Lys Glu Ile Asp Asn Tyr Thr Lys Leu Ile Tyr Ser Leu Ile
155                 645                  650                  655
157 Glu Glu Ser Gln Ile Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu Glu
158         660                  665                  670
160 Leu Asp Lys Trp Ala Asn Leu Trp Asn Trp Phe Asp Ile Ser Asn Trp
161         675                 680                  685
163 Leu Trp Tyr Ile Lys Ile Phe Ile Met Ile Val Gly Gly Leu Val Gly
164         690                 695                  700
166 Leu Arg Ile Val Phe Val Val Leu Ser Ile Val Asn Arg Val Arg Gln
167 705                 710                  715                  720
169 Gly Tyr Ser Pro Leu Ser Phe Gln Thr Arg Leu Pro Ala Pro Arg Gly
170                 725                  730                  735
172 Pro Asp Arg Pro Glu Glu Ile Glu Glu Glu Gly Gly Asp Arg Asp Arg
173         740                  745                  750
175 Asp Arg Ser Gly Leu Leu Val Asp Gly Phe Leu Thr Leu Ile Trp Val
176         755                  760                  765
178 Asp Leu Arg Ser Leu Cys Leu Phe Ser Tyr His Arg Leu Arg Asp Leu
179         770                 775                  780
181 Leu Leu Ile Val Thr Arg Ile Val Glu Leu Leu Gly Arg Arg Gly Trp
182 785                 790                  795                  800
184 Glu Ile Leu Lys Tyr Trp Trp Asn Leu Leu Gln Tyr Trp Ser Gln Glu
185                 805                  810                  815
187 Leu Lys Asn Ser Ala Val Ser Leu Phe Asn Ala Thr Ala Ile Ala Val
188         820                  825                  830
190 Ala Glu Gly Thr Asp Arg Val Ile Glu Val Leu Gln Arg Val Gly Arg
191         835                  840                  845
193 Ala Leu Leu His Ile Pro Thr Arg Ile Arg Gln Gly Leu Glu Arg Ala
194         850                 855                  860
196 Leu Leu
197 865
200 <210> SEQ ID NO: 2
201 <211> LENGTH: 17
202 <212> TYPE: PRT
203 <213> ORGANISM: Human immunodeficiency virus type 1
205 <220> FEATURE:
206 <223> OTHER INFORMATION: segment of R2 strain V3 domain
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209 Lys Ser Ile Pro Met Gly Pro Gly Arg Ala Phe Tyr Thr Thr Gly Gln
210  1               5                  10                  15
212 Ile
216 <210> SEQ ID NO: 3
217 <211> LENGTH: 35
218 <212> TYPE: PRT
219 <213> ORGANISM: Human immunodeficiency virus type 1
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221 <220> FEATURE:
222 <223> OTHER INFORMATION: R2 strain V3 domain
224 <400> SEQUENCE: 3
225 Cys Ser Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Pro Met Gly Pro
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229            20                  25                 30
231 Ala His Cys
232         35
235 <210> SEQ ID NO: 4
236 <211> LENGTH: 35
237 <212> TYPE: PRT
238 <213> ORGANISM: Human immunodeficiency virus type 1
240 <220> FEATURE:
241 <223> OTHER INFORMATION: V3 domain of strain 93TH966.8
243 <400> SEQUENCE: 4
244 Cys Thr Arg Pro Ser Asn Asn Thr Arg Thr Ser Thr Thr Ile Gly Pro
245  1               5                  10                 15
247 Gly Gln Val Phe Tyr Arg Thr Gly Asp Ile Thr Gly Asn Ile Arg Lys
248            20                  25                 30
250 Ala Tyr Cys
251         35
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VERIFICATION SUMMARY
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